

T560X

(1) GENERAL INFORMATION:

(i) APPLICANTS: Boon, Thierry, Van den Eynde, Benoît

(ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Felfe & Lynch
- (B) STREET: 805 Third Avenue
- (C) CITY: New York City
- (D) STATE: New York
- (F) ZIP: 10022

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
- (B) COMPUTER: IBM
- (C) OPERATING SYSTEM: PC-DOS
- (D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/807,043
- (B) FILING DATE: 12-DECEMBER-1991
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/764,364
- (B) FILING DATE: 23-SEPTEMBER-1991

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/728,838
- (B) FILING DATE: 9-JULY-1991

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: 07/705,702
- (B) FILING DATE: 23-May-1991

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Hanson, Norman D.
- (B) REGISTRATION NUMBER: 30,946
- (C) REFERENCE/DOCKET NUMBER: LUD 253.3

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 688-9200
- (B) TELEFAX: (212) 838-3884

- (2) INFORMATION FOR SEQUENCE ID NO: 1:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: singular
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	GAAGATCCTG	60
ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	CAGCCAATGA	GCTTACTGTT	120
CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	AAGTTTGCA	AGTTCCGCCT	ACAGCTCTAG	180
CTTGTGAATT	TGTACCCTTT	CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	240
CCCCCTCCCA	CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTT	GCTCTCCCAG	CATGCATTGT	360
GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	CTAGCTTGCG	ACTCTACTCT	420
TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	ACCCTTTGTG	CC		462

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT	48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly	
5 10 15	
GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA	96
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu	
20 25 30	
GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA	144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr	
35 40 45	
AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG	192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln	
50 55 60	
TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC	240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser	
65 70 75 80	
TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC	288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr	
85 90 95	
GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	336
Asp Asp Glu Asp Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp	
100 105 110	
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG	384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu	
115 120 125	
GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG	432
Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met	
130 135 140	
GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG	480
Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys	
145 150 155 160	
AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC	528
Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe	
165 170 175	

CTG	GTG	TCT	ATA	CCA	GTG	AAC	CCT	AAG	GAA	CAA	ATG	GAG	TGT	AGG	TGT	576
Leu	Val	Ser	Ile	Pro	Val	Asn	Pro	Lys	Glu	Gln	Met	Glu	Cys	Arg	Cys	
			180					185					190			
GAA	AAT	GCT	GAT	GAA	GAG	GTT	GCA	ATG	GAA	GAG	GAA	GAA	GAA	GAA	GAG	624
Glu	Asn	Ala	Asp	Glu	Glu	Val	Ala	Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
		195					200				205					
GAG	GAG	GAG	GAG	GAA	GAG	GAA	ATG	GGA	AAC	CCG	GAT	GGC	TTC	TCA	CCT	672
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Met	Gly	Asn	Pro	Asp	Gly	Phe	Ser	Pro	
210					215					220					225	
TAG																675

- (2) INFORMATION FOR SEQUENCE ID NO: 3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT	GCAAAGCCCA	GAAGAAAGAA	ATGGACAGCG	GAAGAAGTGG	TTGTTTTTTT	60
TTCCCCTTCA	TTAATTTTCT	AGTTTTTAGT	AATCCAGAAA	ATTTGATTTT	GTTCTAAAGT	120
TCATTATGCA	AAGATGTCAC	CAACAGACTT	CTGACTGCAT	GGTGAACTTT	CATATGATAC	180
ATAGGATTAC	ACTTGTACCT	GTTAAAAATA	AAAGTTTGAC	TTGCATAC		228

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG	150
AAGTTTGTCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT	200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA	250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT	300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG	350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG	400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT	450
ACCCTTTGTG CC	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA	504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG	546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC	588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC	630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC	672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG	714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC	756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT	798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA	840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT	924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT	966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG	1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT	1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG	1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT	1134
TAG	1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG	1187
TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA	1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT	1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT	1337
GTAAAAATA AAAGTTTGAC TTGCATAC	1365

(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	50
GAAGATCCTG	ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	100
CAGCCAATGA	GCTTACTGTT	CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	150
AAGTTTGTCA	AGTTCCGCCT	ACAGCTCTAG	CTTGTGAATT	TGTACCCTTT	200
CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	CCCCCTCCCA	250
CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTTT	GCTCTCCCAG	350
CATGCATTGT	GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	400
CTAGCTTGCG	ACTCTACTCT	TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	450
ACCCTTTGTG	CC				462
ATG TCT GAT	AAC AAG AAA	CCA GAC AAA	GCC CAC AGT	GGC TCA	504
GGT GGT GAC	GGT GAT GGG	AAT AGG TGC	AAT TTA TTG	CAC CGG	546
TAC TCC CTG	GAA GAA ATT	CTG CCT TAT	CTA GGG TGG	CTG GTC	588
TTC GCT GTT	GTC ACA ACA	AGT TTT CTG	GCG CTC CAG	ATG TTC	630
ATA GAC GCC	CTT TAT GAG	GAG CAG TAT	GAA AGG GAT	GTG GCC	672
TGG ATA GCC	AGG CAA AGC	AAG CGC ATG	TCC TCT GTC	GAT GAG	714
GAT GAA GAC	GAT GAG GAT	GAT GAG GAT	GAC TAC TAC	GAC GAC	756
GAG GAC GAC	GAC GAC GAT	GCC TTC TAT	GAT GAT GAG	GAT GAT	798
GAG GAA GAA	GAA TTG GAG	AAC CTG ATG	GAT GAT GAA	TCA GAA	840
GAT GAG GCC	GAA GAA GAG	ATG AGC GTG	GAA ATG GGT	GCC GGA	882
GCT GAG GAA	ATG GGT GCT	GGC GCT AAC	TGT GCC T		916
GTGAGTAACC	CGTGGTCTTT	ACTCTAGATT	CAGGTGGGGT	GCATTCTTTA	966
CTCTTGCCCA	CATCTGTAGT	AAAGACCACA	TTTTGGTTGG	GGGTCATTGC	1016
TGGAGCCATT	CCTGGCTCTC	CTGTCCACGC	CTATCCCCGC	TCCTCCCATC	1066
CCCCACTCCT	TGCTCCGCTC	TCTTTCCTTT	TCCCACCTTG	CCTCTGGAGC	1116
TTCACTCCAT	CCTGCTCTGC	TCCCTTTCCC	CTTTGCTCTC	CTTGCTCCCC	1166
TCCCCCTCGG	CTCAACTTTT	CGTGCCTTCT	GCTCTCTGAT	CCCCACCCTC	1216
TTCAAGGCTTC	CCCATTTGCT	CCTCTCCCGA	AACCCTCCCC	TTCCCTGTTCC	1266
CCTTTTCGCG	CCTTTTCTTT	CCTGCTCCCC	TCCCCCTCCC	TATTTACCTT	1316
TCACCAGCTT	TGCTCTCCCT	GCTCCCCTCC	CCCTTTTGCA	CCTTTTCTTT	1366
TCCTGCTCCC	CTCCCCCTCC	CCTCCCTGTT	TACCCTTCAC	CGCTTTTCCT	1416
CTACCTGCTT	CCCTCCCCCT	TGCTGCTCCC	TCCCTATTTG	CATTTTCGGG	1466
TGCTCCTCCC	TCCCCCTCCC	CCTCCCTCCC	TATTTGCATT	TTCGGGTGCT	1516
CCTCCCTCCC	CCTCCCCAGG	CCTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	1566
TTGGTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCCTGGCAC	1616
TCACTCTGTA	GACCAGGCTG	GCCTCAAAC	CAGAAATCTG	CCTGCCTCTG	1666
CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
GCCTTTCCTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
AACTCCCCTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCTGT	1816
TTCCCTTCCG	GCACCCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
CCTCCCCCTC	TTTGCTCGAC	TTTTAGCAGC	CTTACCTCTC	CCTGCTTTCT	1916
GCCCCGTTCC	CCTTTTTTGT	GCCTTTCCTC	CTGGCTCCCC	TCCACCTTCC	1966

AGCTCACCTT	TTTGTTTGTT	TGGTTGTTTG	GTTGTTTGGT	TTGCTTTTTT	2016
TTTTTTTTTT	GCACCTTGTT	TTCCAAGATC	CCCCTCCCCC	TCCGGCTTCC	2066
CCTCTGTGTG	CCTTTCCTGT	TCCCTCCCCC	TCGCTGGCTC	CCCCTCCCTT	2116
TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
CTTTTCTAGA	CTCCCCCCTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
CCTGACCCTG	CTCCCCCTTC	CCTCCCAGCT	CCCCCTCTT	TTCCCACCTC	2266
CCTTTCTCCA	GCCTGTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCACT	2316
TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
GACTTCCTCT	CCAGCCGCCC	AGTTCCTGCT	AGTCCTGGAG	TCTTTCCTGC	2416
CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCTT	2466
ATGTGTCTCT	CTTCCTATCT	ATCCCTTCCT	TTCTGTCCCC	TCTCCTCTGT	2516
CCATCACCTC	TCTCCTCCCT	TCCCTTTCCT	CTCTCTTCCA	TTTTCTTCCA	2566
CCTGCTTCTT	TACCCTGCCT	CTCCCATGCT	CCTCTTACCT	TTATGCCCCAT	2616
TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666
ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTATAG	CCCTCTACTC	2766
TACTTGATCT	TCTCTCCTCT	CCACATAACC	TTTTTCCTTT	CCACCCTGCC	2816
CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCAAA	ATCAGCAGGA	2916
AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
AAGTGGCTCC	TATAACCCTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016
CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166
TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTTA	3266
GGCTAAAGAT	ACTTGGAACC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTTCTT	3316
TTGCTAAAAT	ATTCTTTCTC	ACATATTCAT	ATTCTCCAG		3355
GT GTT CCT	GGC CAT CAT	TTA AGG AAG	AAT GAA GTG	AAG TGT	3396
AGG ATG ATT	TAT TTC TTC	CAC GAC CCT	AAT TTC CTG	GTG TCT	3438
ATA CCA GTG	AAC CCT AAG	GAA CAA ATG	GAG TGT AGG	TGT GAA	3480
AAT GCT GAT	GAA GAG GTT	GCA ATG GAA	GAG GAA GAA	GAA GAA	3522
GAG GAG GAG	GAG GAG GAA	GAG GAA ATG	GGA AAC CCG	GAT GGC	3564
TTC TCA CCT	TAG				3576
GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCCTAACA	TATGCCTGTA	3626
GCTAAGAGCA	TCTTTTTTAAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
TCTTTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA	3726
CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAATTAT	TATTTTGTCTG	3976
TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT	4026
CTTAAAATTT	CCTTCATCTT	TAATTTTCCT	TAACCTTTAGT	TTTTTTCACT	4076
TAGAATTCAA	TTCAAATTCT	TAATTCAATC	TTAATTTTTTA	GATTTCTTAA	4126
AATGTTTTTT	AAAAAAAATG	CAAATCTCAT	TTTTAAGAGA	TGAAAGCAGA	4176
GTAAGTGGGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTGC	4276
CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
ATAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGAAAT	4376
ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATAAAA	TTGGCAAGAA	4426
AGTCAGGAGT	GTATTCTAAT	AAGTGTGCT	TATCTCTTAT	TTTCTTCTAC	4476
AGTTGCAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTTT	4526
TTTTTTCCCC	TTCATTAATT	TTCTAGTTTT	TAGTAATCCA	GAAAATTTGA	4576

TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT
GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA
AATAAAAGTT TGACTTGCAT AC

4626
4676
4698

- (2) INFORMATION FOR SEQUENCE ID NO: 6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu
5

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(2) INFORMATION FOR SEQUENCE ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
GGGGTCATCC	ACTGCATGAG	AGTGGGGATG	TCACAGAGTC	CAGCCCACCC	100
TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCTGAG	150
GGCCCGTGGA	TTCCTCTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAGGACACAT	AGGACTCCAC	AGAGTCTGGC	CTCACCTCCC	TACTGTCAGT	350
CCTGTAGAAT	CGACCTCTGC	TGGCCGGCTG	TACCCTGAGT	ACCCTCTCAC	400
TTCCTCCTTC	AGGTTTTTCAG	GGGACAGGCC	AACCCAGAGG	ACAGGATTCC	450
CTGGAGGCCA	CAGAGGAGCA	CCAAGGAGAA	GATCTGTAAG	TAGGCCTTTG	500
TTAGAGTCTC	CAAGGTTTCAG	TTCTCAGCTG	AGGCCTCTCA	CACACTCCCT	550
CTCTCCCCAG	GCCTGTGGGT	CTTCATTGCC	CAGCTCCTGC	CCACACTCCT	600
GCCTGCTGCC	CTGACGAGAG	TCATCATGTC	TCTTGAGCAG	AGGAGTCTGC	650
ACTGCAAGCC	TGAGGAAGCC	CTTGAGGGCCC	AACAAGAGGC	CCTGGGCGTG	700
GTGTGTGTGC	AGGCTGCCAC	CTCCTCCTCC	TCTCCTCTGG	TCCTGGGCAC	750
CCTGGAGGAG	GTGCCCACTG	CTGGGTCAAC	AGATCCTCCC	CAGAGTCCTC	800
AGGGAGCCTC	CGCCTTTCCC	ACTACCATCA	ACTTCACTCG	ACAGAGGCAA	850
CCCAGTGAGG	GTTCCAGCAG	CCGTGAAGAG	GAGGGGCCAA	GCACCTCTTG	900
TATCCTGGAG	TCCTTGTTCC	GAGCAGTAAT	CACTAAGAAG	GTGGCTGATT	950
TGGTTGGTTT	TCTGCTCCTC	AAATATCGAG	CCAGGGAGCC	AGTCACAAAG	1000
GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTCTCTGA	1050
GATCTTCGGC	AAAGCCTCTG	AGTCCTTGCA	GCTGGTCTTT	GGCATTGACG	1100
TGAAGGAAGC	AGACCCACCC	GGCCACTCCT	ATGTCCTTGT	CACCTGCCTA	1150
GGTCTCTCCT	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCAAGAC	1200
AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
CTCCTGAGGA	GGAAATCTGG	GAGGAGCTGA	GTGTGATGGA	GGTGTATGAT	1300
GGGAGGGAGC	ACAGTGCCTA	TGGGGAGCCC	AGGAAGCTGC	TCACCCAAGA	1350
TTTGGTGACG	GAAAAGTACC	TGGAGTACGG	CAGGTGCCGG	ACAGTGATCC	1400
CGCACGCTAT	GAGTTCCTGT	GGGGTCCAAG	GGCCCTCGCT	GAAACCAGCT	1450
ATGTGAAAGT	CCTTGAGTAT	GTGATCAAGG	TCAGTGCAAG	AGTTCGCTTT	1500
TTCTTCCCAT	CCCTGCGTGA	AGCAGCTTTG	AGAGAGGAGG	AAGAGGGAGT	1550
CTGAGCATGA	GTTGCAGCCA	AGGCCAGTGG	GAGGGGGACT	GGGCCAGTGC	1600
ACCTTCCAGG	GCCGCGTCCA	GCAGCTTCCC	CTGCCTCGTG	TGACATGAGG	1650
CCCATTCTTC	ACTCTGAAGA	GAGCGGTCAG	TGTTCTCAGT	AGTAGGTTTC	1700
TGTTCTATTG	GGTGACTTGG	AGATTTATCT	TTGTTCTCTT	TTGGAATTGT	1750
TCAAATGTTT	TTTTTTAAAG	GATGGTTGAA	TGAACTTCAG	CATCCAAGTT	1800
TATGAATGAC	AGCAGTCACA	CAGTTCTGTG	TATATAGTTT	AAGGGTAAGA	1850
GTCTTGTGTT	TTATTTCAGAT	TGGGAAATCC	ATTCTATTTT	GTGAATTGGG	1900
ATAATAACAG	CAGTGGAATA	AGTACTTAGA	AATGTGAAAA	ATGAGCAGTA	1950
AAATAGATGA	GATAAAGAAC	TAAAGAAATT	AAGAGATAGT	CAATTCTTGC	2000
CTTATACCTC	AGTCTATTCT	GTAAAATTTT	TAAAGATATA	TGCATACCTG	2050

GATTCCTTG	GCTTCTTTGA	GAATGTAAGA	GAAATTAAAT	CTGAATAAAG	2100
AATTCTTCCT	GTTCACTGGC	TCTTTTCTTC	TCCATGCACT	GAGCATCTGC	2150
TTTTTGGAAG	GCCCTGGGTT	AGTAGTGGAG	ATGCTAAGGT	AAGCCAGACT	2200
CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGCAGT	CACGTAATCG	2250
AGGTGGCAAG	ATGTCCTCTA	AAGATGTAGG	GAAAAGTGAG	AGAGGGGTGA	2300
GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGA	GTGTCAATGC	CCTGAGCTGG	2350
GGCATTTTGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGGGGG	AGCTGATTGT	2400
AATGATCTTG	GGTGGATCC				2419

(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5688 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCGGGGCAC	CACTGGCATC	CCTCCCCCTA	CCACCCCCAA	TCCCTCCCTT	50
TACGCCACCC	ATCCAAACAT	CTTCACGCTC	ACCCCCAGCC	CAAGCCAGGC	100
AGAATCCGGT	TCCACCCCTG	CTCTCAACCC	AGGGAAGCCC	AGGTGCCCAG	150
ATGTGACGCC	ACTGACTTGA	GCATTAGTGG	TTAGAGAGAA	GCGAGGTTTT	200
CGGTCTGAGG	GGCGGCTTGA	GATCGGTGGA	GGGAAGCGGG	CCCAGCTCTG	250
TAAGGAGGCA	AGGTGACATG	CTGAGGGAGG	ACTGAGGACC	CACTTACCCC	300
AGATAGAGGA	CCCCAAATAA	TCCCTTCATG	CCAGTCCTGG	ACCATCTGGT	350
GGTGGACTTC	TCAGGCTGGG	CCACCCCCAG	CCCCCTTGCT	GCTTAAACCA	400
CTGGGGACTC	GAAGTCAGAG	CTCCGTGTGA	TCAGGGAAGG	GCTGCTTAGG	450
AGAGGGCAGC	GTCCAGGCTC	TGCCAGACAT	CATGCTCAGG	ATTCTCAAGG	500
AGGGCTGAGG	GTCCCTAAGA	CCCCACTCCC	GTGACCCAAC	CCCCACTCCA	550
ATGCTCACTC	CCGTGACCCA	ACCCCCTCTT	CATTGTCAAT	CCAACCCCCA	600
CCCCACATCC	CCCACCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCCAGCC	650
ATTCCACCCT	CACCCCCACC	CCCACCCCCA	CGCCCACTCC	CACCCCCACC	700
CAGGCAGGAT	CCGGTTCCCG	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
AGGGACGGCG	TAGAGTTCGG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCGCC	ACTCCAAATA	900
GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCACC	950
CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
CCTTGAGAGA	CACCAGGTTT	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
ACTCCAATCC	CCACTCCAC	CCCATTGCA	TTCCCATTC	CCACCCAACC	1200
CCCATCTCCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
CCTGACCACC	ACCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
TCACCCTCAC	TGCCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
CCCATCGCCT	CCCCCATTCT	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
CCAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCACTGACT	TGAACCTCAC	1450
AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
ATCCACTGAG	GGGAGTGGTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
GTCTCAGCTG	GACCACCCCC	CGTCCCGTCC	CACTGCCACT	TAACCCACAG	1700
GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
ACCCTGGGAG	GGAAGTGAAG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
CACCGCCACC	CCACTCACAT	TCCCATACTT	ACCCCCTACC	CCCAACCTCA	1900
TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000

GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACGCGG	AGGAAGAGGA	2200
GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
CTGTCCCCTT	TTAGTAGCTC	TAGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
TTCCATTCTC	ACTTGTAACA	CAGGCAGGAA	GTGGGGGGGC	CCTCAGGGAG	2550
ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
GGTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTGAGC	CCTGGACACC	2700
TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTCCAGA	TCTGGGGCAG	2750
GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
GAACATGAGG	GAGGACTGAG	GGTACCCAG	GACCAGAACA	CTGAGGGAGA	2900
CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCAGAG	AGCATGGGCT	2950
GGGCCGTCTG	CCGAGGTCCCT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
ACGGGGAGGC	CTTGCTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCCTCCT	GTCCCTCCAT	3200
TCCTTATCAT	GGATGTGAAC	TCTTGATTG	GATTTCTCAG	ACCAGCAAAA	3250
GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
CACCCCTCCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400
CTGAGGGCCC	GTGGATTCCCT	CTTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3450
GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3500
GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3550
TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600
TCAGTCCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCT	3650
CTCACTTCCT	CCTTCAGGTT	TTCAGGGGAC	AGGCCAACCC	AGAGGACAGG	3700
ATTCCCTGGA	GGCCACAGAG	GAGCACCAAG	GAGAAGATCT	GTAAGTAGGC	3750
CTTTGTTAGA	GTCTCCAAGG	TTCAGTTCTC	AGCTGAGGCC	TCTCACACAC	3800
TCCCTCTCTC	CCCAGGCCTG	TGGGTCTTCA	TTGCCCAGCT	CCTGCCCACA	3850
CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3880
ATG TCT CTT	GAG CAG AGG	AGT CTG CAC	TGC AAG CCT	GAG GAA	3922
GCC CTT GAG	GCC CAA CAA	GAG GCC CTG	GGC CTG GTG	TGT GTG	3964
CAG GCT GCC	ACC TCC TCC	TCT CCT CTG	GTC CTG GGC	ACC	4006
CTG GAG GAG	GTG CCC ACT	GCT GGG TCA	ACA GAT CCT	CCC CAG	4048
AGT CCT CAG	GGA GCC TCC	GCC TTT CCC	ACT ACC ATC	AAC TTC	4090
ACT CGA CAG	AGG CAA CCC	AGT GAG GGT	TCC AGC AGC	CGT GAA	4132
GAG GAG GGG	CCA AGC ACC	TCT TGT ATC	CTG GAG TCC	TTG TTC	4174
CGA GCA GTA	ATC ACT AAG	AAG GTG GCT	GAT TTG GTT	GGT TTT	4216
CTG CTC CTC	AAA TAT CGA	GCC AGG GAG	CCA GTC ACA	AAG GCA	4258
GAA ATG CTG	GAG AGT GTC	ATC AAA AAT	TAC AAG CAC	TGT TTT	4300
CCT GAG ATC	TTC GGC AAA	GCC TCT GAG	TCC TTG CAG	CTG GTC	4342
TTT GGC ATT	GAC GTG AAG	GAA GCA GAC	CCC ACC GGC	CAC TCC	4384
TAT GTC CTT	GTC ACC TGC	CTA GGT CTC	TCC TAT GAT	GGC CTG	4426
CTG GGT GAT	AAT CAG ATC	ATG CCC AAG	ACA GGC TTC	CTG ATA	4468
ATT GTC CTG	GTC ATG ATT	GCA ATG GAG	GGC GGC CAT	GCT CCT	4510
GAG GAG GAA	ATC TGG GAG	GAG CTG AGT	GTG ATG GAG	GTG TAT	4552

GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC AGG AAG CTG	4594
CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG GAG TAC GGC	4636
AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT TCC TGT GGG	4678
GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA	4711
AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC	4750
GCTTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA GGAGGAAGAG	4800
GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG GGACTGGGCC	4850
AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCCTGCC TCGTGTGACA	4900
TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTT TCAGTAGTAG	4950
GTTTCTGTTC TATTGGGTGA CTTGGAGATT TATCTTTGTT CTCTTTTGGA	5000
ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC TTCAGCATCC	5050
AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT AGTTTAAGGG	5100
TAAGAGTCTT GTGTTTTATT CAGATTGGGA AATCCATTCT ATTTTGTGAA	5150
TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT GAAAAATGAG	5200
CAGTAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG ATAGTCAATT	5250
CTTGCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTAAAG ATATATGCAT	5300
ACCTGGATTT CCTTGCTTC TTTGAGAATG TAAGAGAAAT TAAATCTGAA	5350
TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT GCACTGAGCA	5400
TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT AAGGTAAGCC	5450
AGACTCATAC CCACCCATAG GGTCTAGAG TCTAGGAGCT GCAGTCACGT	5500
AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA GTGAGAGAGG	5550
GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC AATGCCCTGA	5600
GCTGGGGCAT TTTGGGCTTT GGGAACTGC AGTTCCTTCT GGGGGAGCTG	5650
ATTGTAATGA TCTTGGGTGG ATCC	5688

(2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCCACCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGCCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTCGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCGC	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACCGCAG	350
GGAACCTCTG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCCAAC	500
ACCAACCCCA	CCCCCATCCC	TCAAACACCA	ACCCACCCCC	CAAACCCCAT	550
TCCCATCTCC	TCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCACTG	TACCCCTGTC	800
TCAAACCTGAG	CCACCTTTTC	ATTCAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCCACTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
AAGAGGGAGG	ACTGAGGGGA	CCTTGAGATC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTCGAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTC	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAAGAGGA	GCTGTCTGCT	CATTTTCAGG	1300
GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTTACCCCTA	GAACCAAAGG	GGTCAGCCCT	1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGTCCTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGCCC	CTCTGGTCGA	CAGATGCAGT	GGTTCTAGGA	TCTGCCAAGC	1550
ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGC	GTTACTTCAG	1650
AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCTCCATTAT	CTGGGATCTT	1700
TGATGTCAGG	GAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750
GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTGAC	ATCTCTCGTT	1850
GTCCTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCCTCTA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000

CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACTGAAGGC	CCGTGCATTC	CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTTA	AGGAGAAGAT	2450
CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT	GCCCCGACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723
TCT ACT CTA	GTG GAA GTT	ACC CTG GGG	GAG GTG CCT	GCT GCC	2765
GAC TCA CCG	AGT CCT CCC	CAC AGT CCT	CAG GGA GCC	TCC AGC	2807
TTC TCG ACT	ACC ATC AAC	TAC ACT CTT	TGG AGA CAA	TCC GAT	2849
GAG GGC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGA	ATG TTT	2891
CCC GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA ATC AGT	AGG AAG	2933
ATG GTT GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	2975
AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GAG AGT	GTC CTC	3017
AGA AAT TGC	CAG GAC TTC	TTT CCC GTG	ATC TTC AGC	AAA GCC	3059
TCC GAG TAC	TTG CAG CTG	GTC TTT GGC	ATC GAG GTG	GTG GAA	3101
GTG GTC CCC	ATC AGC CAC	TTG TAC ATC	CTT GTC ACC	TGC CTG	3143
GGC CTC TCC	TAC GAT GGC	CTG CTG GGC	GAC AAT CAG	GTC ATG	3185
CCC AAG ACA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	3227
ATA GAG GGC	GAC TGT GCC	CCT GAG GAG	AAA ATC TGG	GAG GAG	3269
CTG AGT ATG	TTG GAG GTG	TTT GAG GGG	AGG GAG GAC	AGT GTC	3311
TTC GCA CAT	CCC AGG AAG	CTG CTC ATG	CAA GAT CTG	GTG CAG	3353
GAA AAC TAC	CTG GAG TAC	CGG CAG GTG	CCC GGC AGT	GAT CCT	3395
GCA TGC TAC	GAG TTC CTG	TGG GGT CCA	AGG GCC CTC	ATT GAA	3437
ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ACA CTA AAG	ATC GGT	3479
GGA GAA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAA	CGG GCT	3521
TTG AGA GAG	GGA GAA GAG	TGA			3542
GTCTCAGCAC	ATGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	3592
GCACCTTCCA	GGGCCCCATC	CATTAGCTTC	CACTGCCTCG	TGTGATATGA	3642
GGCCCATTC	TGCCTCTTTG	AAGAGAGCAG	TCAGCATTTCT	TAGCAGTGAG	3692
TTTCTGTTCT	GTTGGATGAC	TTTGAGATTT	ATCTTTCTTT	CCTGTTGGAA	3742
TTGTTCAAAT	GTTCCTTTTA	ACAAATGGTT	GGATGAACTT	CAGCATCCAA	3792
GTTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGGG	3842
TAAGAGTCCT	GTTTTTTTATT	CAGATTGGGA	AATCCATTCC	ATTTTGTGAG	3892
TTGTCACATA	ATAACAGCAG	TGGAATATGT	ATTTGCCCTAT	ATTGTGAACG	3942
AATTAGCAGT	AAAATACATG	ATACAAGGAA	CTCAAAAGAT	AGTTAATTCT	3992
TGCCTTATAC	CTCAGTCTAT	TATGTAAAAT	TAAAAATATG	TGTATGTTTT	4042
TGCTTCTTTG	AGAATGCAAA	AGAAATTAAA	TCTGAATAAA	TTCTTCCTGT	4092
TCAGTGCTC	ATTTCTTTAC	CATTCACTCA	GCATCTGCTC	TGTGGAAGGC	4142
CCTGGTAGTA	GTGGG				4157

- (2) INFORMATION FOR SEQUENCE ID NO: 10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 662 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-21 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG	50
GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA	100
AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCAC ACTCCCGCCT	150
GTTGCCCTGA CCAGAGTCAT C	171
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	213
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	255
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	297
TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	339
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	381
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	423
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	465
CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG	507
GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	549
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC	591
GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT	633
TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA	675
GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG	717
GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	801
AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	1011
ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	1053
GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	1095
TTG AGA GAG GGG GAA GAG TGA	1116
GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	1166
GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA	1216
GGCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTTCT TAGTAGTGGG	1266
TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG	1316
TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	1366
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG	1416
TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA	1466
TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC	1516
GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG	1566
ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA	1616
ACCAGGATTT CCTTGACTTC TTTG	1640

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-31 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA	CCCCAGTAGA	GTGGGGACCT	CACAGAGTCT	GGCCAACCCT	50
CCTGACAGTT	CTGGGAATCC	GTGGCTGCGT	TTGCTGTCTG	CACATTGGGG	100
GCCCGTGGAT	TCCTCTCCCA	GGAATCAGGA	GCTCCAGGAA	CAAGGCAGTG	150
AGGACTTGGT	CTGAGGCAGT	GTCCTCAGGT	CACAGAGTAG	AGGGGgCTCA	200
GATAGTGCCA	ACGGTGAAGG	TTTGCCTTGG	ATTCAAACCA	AGGGCCCCAC	250
CTGCCCCAGA	ACACATGGAC	TCCAGAGCGC	CTGGCCTCAC	CCTCAATACT	300
TTCAGTCCTG	CAGCCTCAGC	ATGCGCTGGC	CGGATGTACC	CTGAGGTGCC	350
CTCTCACTTC	CTCCTTCAGG	TTCTGAGGGG	ACAGGCTGAC	CTGGAGGACC	400
AGAGGCCCCC	GGAGGAGCAC	TGAAGGAGAA	GATCTGTAAG	TAAGCCTTTG	450
TTAGAGCCTC	CAAGGTTCCA	TTCAGTACTC	AGCTGAGGTC	TCTCACATGC	500
TCCCTCTCTC	CCCAGGCCAG	TGGGTCTCCA	TTGCCCAGCT	CCTGCCCCACA	550
CTCCCGCCTG	TTGCCCTGAC	CAGAGTCATC			580
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	622
GGC CTT GAG	GCC CGA GGA	GAg GCC CTG	GGC CTG GTG	GGT GCG	664
CAG GCT CCT	GCT ACT GAG	GAG CAG GAG	GCT GCC TCC	TCC TCT	706
TCT AGT GTA	GTT GAA GTC	ACC CTG GGG	GAG GTG CCT	GCT GCC	748
GAG TCA CCA	GAT CCT CCC	CAG AGT CCT	CAG GGA GCC	TCC AGC	790
CTC CCC ACT	ACC ATG AAC	TAC CCT CTC	TGG AGC CAA	TCC TAT	832
GAG GAC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGC	ACC TTC	874
CCT GAC CTG	GAG TCT GAG	TTC CAA GCA	GCA CTC AGT	AGG AAG	916
GTG GCC AAG	TTG GTT CAT	TTT CTG CTC			943

(2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1067 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singular
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA	39
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG	81
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA	123
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT	165
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT	207
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC	249
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG	291
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC	333
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG	375
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT	417
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC	459
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG	501
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT	543
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG	585
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA	627
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	669
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG	719
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG	769
GCCCATCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG	819
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA	869
ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA	919
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT	969
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT	1019
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC	1067

- (2) INFORMATION FOR SEQUENCE ID NO: 14:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-5 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT	50
AAGCCTTTGT TAGAGCCTCC AAGGTTCACT TTTTAGCTGA GGCTTCTCAC	100
ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC AGCTCCTGCC	150
CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC	184
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	226

- (2) INFORMATION FOR SEQUENCE ID NO: 15:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-6 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TAT	TTC	TTT	CCT	GTG	ATC	TTC	AGC	AAA	GCT	TCC	GAT	TCC	TTG	42
CAG	CTG	GTC	TTT	GGC	ATC	GAG	CTG	ATG	GAA	GTG	GAC	CCC	ATC	84
GGC	CAC	GTG	TAC	ATC	TTT	GCC	ACC	TGC	CTG	GGC	CTC	TCC	TAC	126
GAT	GGC	CTG	CTG	GGT	GAC	AAT	CAG	ATC	ATG	CCC	AGG	ACA	GGC	168
TTC	CTG	ATA	ATC	ATC	CTG	GCC	ATA	ATC	GCA	AGA	GAG	GGC	GAC	210
TGT	GCC	CCT	GAG	GAG										225

- (2) INFORMATION FOR SEQUENCE ID NO: 16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 166 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: singular
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-7 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG	42
TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC	84
CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC	126
TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A	166

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